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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,421

DATE: 05/30/2002

TIME: 10:06:16

Input Set : A:\Hayak-9.app

Output Set : N:\CRF3\05302002\J076421.raw

C--> 3 <110> APPLICANT: WADA, MANABU  
4 WADA, NAKO  
6 <120> TITLE OF INVENTION: ANTI-HIV AGENTS  
8 <130> FILE REFERENCE: HAYAK-9  
10 <140> CURRENT APPLICATION NUMBER: 10/076,421  
11 <141> CURRENT FILING DATE: 2002-05-17  
13 <150> PRIOR APPLICATION NUMBER: JP 2001-42655  
14 <151> PRIOR FILING DATE: 2001-02-20  
16 <150> PRIOR APPLICATION NUMBER: JP 2001-184284  
17 <151> PRIOR FILING DATE: 2001-06-19  
19 <160> NUMBER OF SEQ ID NOS: 5  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1296  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (1)..(1293)  
32 <400> SEQUENCE: 1  
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34 Met Arg Ala Leu Leu Ala Arg Leu Leu Cys Val Leu Val Val Ser  
35 1 5 10 15  
37 gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac 96  
38 Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp  
39 20 25 30  
41 tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att 144  
42 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile  
43 35 40 45  
45 cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata 192  
46 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile  
47 50 55 60  
49 gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga 240  
50 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly  
51 65 70 75 80  
53 aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct 288  
54 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser  
55 85 90 95  
57 gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt 336  
58 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
59 100 105 110  
61 cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg 384  
62 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg

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63	115	120	125	
65	agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432		
66	Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln			
67	130	135	140	
69	gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480		
70	Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro			
71	145	150	155	160
73	cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528		
74	Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg			
75	165	170	175	
77	ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576		
78	Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp			
79	180	185	190	
81	ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624		
82	Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val			
83	195	200	205	
85	tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672		
86	Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His			
87	210	215	220	
89	tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720		
90	Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly			
91	225	230	235	240
93	cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768		
94	Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val			
95	245	250	255	
97	gaa aac cta atc cta cac aag gac tac agc gct gac acg ctt gct cac	816		
98	Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His			
99	260	265	270	
101	cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864		
102	His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys			
103	275	280	285	
105	gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat	912		
106	Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr			
107	290	295	300	
109	aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa	960		
110	Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys			
111	305	310	315	320
113	gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt	1008		
114	Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val			
115	325	330	335	
117	gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc	1056		
118	Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly			
119	340	345	350	
121	tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa	1104		
122	Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys			
123	355	360	365	
125	aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc	1152		
126	Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu			
127	370	375	380	

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129  caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt      1200
130  Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
131  385                      390                      395                      400
133  gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta      1248
134  Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
135                      405                      410                      415
137  ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc tga      1296
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142  <210> SEQ ID NO: 2
143  <211> LENGTH: 431
144  <212> TYPE: PRT
145  <213> ORGANISM: Homo sapiens
147  <400> SEQUENCE: 2
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151  Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
152                      20                      25                      30
154  Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
155                      35                      40                      45
157  His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
158                      50                      55                      60
160  Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
161    65                      70                      75                      80
163  Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
164                      85                      90                      95
166  Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
167                      100                     105                     110
169  Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
170                      115                     120                     125
172  Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
173    130                     135                     140
175  Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
176    145                     150                     155                     160
178  Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
179                      165                      170                      175
181  Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
182                      180                      185                      190
184  Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
185                      195                      200                      205
187  Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
188    210                     215                     220
190  Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
191    225                     230                     235                     240
193  Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
194                      245                      250                      255
196  Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
197                      260                      265                      270
199  His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys

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200          275          280          285
202 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
203          290          295          300
205 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
206 305          310          315          320
208 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
209          325          330          335
211 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
212          340          345          350
214 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
215          355          360          365
217 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
218          370          375          380
220 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
221 385          390          395          400
223 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
224          405          410          415
226 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
227          420          425          430
231 <210> SEQ ID NO: 3
232 <211> LENGTH: 4
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 3
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242 <211> LENGTH: 12
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244 <213> ORGANISM: Homo sapiens
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252 <211> LENGTH: 10
253 <212> TYPE: PRT
254 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 5
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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date